

SEQ ID NO:1

Tc	MRKSVC PKQKFFFSAFPFFFFFCVFPLISRTGQEKLFDQKY <u>KI</u> <u>I</u> KGEKKKKNQRANRREHQHQXREIMRFNNNS	75
Tc	FTCIDMHTEGEAAR <u>I</u> <u>V</u> <u>T</u> <u>S</u> <u>G</u> <u>L</u> <u>H</u> <u>P</u> <u>I</u> <u>P</u> <u>G</u> <u>S</u> <u>N</u> MAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF	150
Tc	MDTGGYLNMCGHNSIAAVTRAAVETGIVSVPAK <u>A</u> <u>T</u> <u>N</u> <u>V</u> <u>P</u> <u>V</u> <u>L</u> <u>D</u> <u>T</u> <u>P</u> <u>A</u> <u>G</u> <u>L</u> <u>V</u> <u>R</u> <u>G</u> <u>T</u> <u>A</u> <u>H</u> <u>L</u> <u>Q</u> <u>S</u> <u>G</u> <u>T</u> <u>E</u> <u>S</u> <u>V</u> <u>N</u> <u>A</u> <u>S</u> <u>I</u> <u>I</u> <u>N</u> <u>V</u> <u>P</u> <u>S</u> <u>F</u> <u>L</u> <u>Y</u> <u>Q</u>	225
Tc	QDVVVVLPKPYGEVR <u>V</u> <u>D</u> <u>I</u> <u>A</u> <u>F</u> <u>G</u> <u>G</u> <u>N</u> <u>F</u> <u>A</u> <u>I</u> <u>V</u> <u>P</u> <u>A</u> <u>E</u> <u>Q</u> <u>L</u> <u>G</u> <u>I</u> <u>D</u> <u>I</u> <u>S</u> <u>V</u> <u>Q</u> <u>N</u> <u>L</u> <u>S</u> <u>R</u> <u>L</u> <u>Q</u> <u>E</u> <u>A</u> <u>G</u> <u>E</u> <u>L</u> <u>R</u> <u>T</u> <u>E</u> <u>I</u> <u>N</u> <u>R</u> <u>S</u> <u>V</u> <u>K</u> <u>V</u> <u>Q</u> <u>H</u> <u>P</u> <u>Q</u> <u>L</u> <u>H</u> <u>I</u> <u>N</u> <u>T</u> <u>V</u> <u>D</u> <u>C</u>	300
Tc	VEIYGPPTNPEANY <u>K</u> <u>N</u> <u>V</u> <u>V</u> <u>I</u> <u>F</u> <u>G</u> <u>N</u> <u>R</u> <u>Q</u> <u>A</u> <u>D</u> <u>R</u> SPCGT <u>S</u> <u>T</u> <u>S</u> <u>A</u> <u>K</u> <u>M</u> <u>A</u> <u>T</u> <u>L</u> <u>Y</u> <u>A</u> <u>K</u> <u>G</u> <u>Q</u> <u>L</u> <u>R</u> <u>I</u> <u>G</u> <u>E</u> <u>T</u> <u>F</u> <u>V</u> <u>Y</u> <u>E</u> <u>S</u> <u>I</u> <u>L</u> <u>G</u> <u>S</u> <u>L</u> <u>F</u> <u>Q</u> <u>G</u> <u>R</u> <u>V</u> <u>--</u> <u>L</u> <u>G</u> <u>E</u> <u>E</u>	371
Tc	RIPGVKVVPVKDAEEGMLVVTAEITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*	423

SEQ ID NO:2

Tc	RTGQEKL _{LP} DQKY <u>KI</u> I KGEKKEKKRNQRANRREHQQKREIMRFKKS	75
Tc	FTCIDMHTEGEAARI <u>VT</u> SGLPHIPGSNMAEK KAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLG MVF	150
Tc	MDTGGYLNMCGHNSIAAVTAAVETGIVSVPAK <u>ATNVPVVLDT</u> PAGLVRGTAHLQSGETEVSNASIINVPSFLYQ	225
Tc	QDVVVVLPKPYGEVR <u>VDIA</u> FCCGNFFAIVPAAEQLGIDISVQNLRLQEA ELLRT EINRSVKVQHPQLPHINTVDC	300
Tc	VEIYGPPTNPEANY <u>KNVVIFGNRQADR</u> SPCGT GTS _{AK} <u>MLYAKGQLRIGETFVYESILGSLFQGRV--LGEE</u>	371
Tc	RIPGVKVPVTKD AEEGMLVV TAEITGKA FIMGNTMLFDPTDFKNGFTLKQ*	423

SEQ ID NO:3

Tc MRKSVC?KQKFFFSAFPFFFFFCVFP LIS

SEQUENCE ID NO.4

75
150
225
300
375
425

SEQUENCE ID NO:5

Cs	-----	-MNFNSKG	6	
Cs	IHAIDSHTMGEPTRIVVGGIPQINGETMAACKKYLEDNLDYVRTALMHEPRGHNDMFGSIITSSNNKEADFGIIF		31	
Cs	MDGGGYLNMCGHGSIGAATVAVETGMVENVEPVTNIN--MEAPAGLIKAKVMVEN--EKVKEVSVITNVPSFLYM		151	
Cs	EDAKLEVPSLNKTITFDISFGGSFFAIIAKELGVKVETSQVDVLKKLGIEIRDLINEKIKVQHPELEHIKTVDL		226	
Cs	VEIYDEPSNPEATYKNVVIFGQQQVDR	SPCGT	GTSAKLATLYKKGHLKIDEKEVYESITGTMFKGRV--LEET	297
Cs	KVGEFD-----AIIPEITGGAYITGENHEVIDPEDPLKYGFTV*--	335		

SEQ ID NO:6

Pa	-----	NQR	3
Pa	I R I I D S H T G G E P T R L V I G G F P D L G Q G D M A E R R R L L G E R H D A W R A A C I L E P R G S D V I V G A L L C A P V D P E A C A G V I F		73
Pa	F N N S G Y L G M C G H G T I G L V A S L A H L G R I G P G V ----- H R I E T P V G E V E A T L H ----- E D G S V S V R N V P A Y R Y R		140
Pa	R Q V S V E V P G I - G R V S G D I A W G G N W F F L V A G H -- G Q R L A G O N L D A L T A Y T V A V Q Q A L D D ----- Q D I R G E D G G A I D H		206
Pa	I E L F A D -- D P H A D S R N F V L C P G K A Y D R S P C G T G T S A K L A C L A A D G K L L P G Q P W R Q A S V I G S Q F E G R Y E W L Q Q		279
Pa	P G G P I V P T I R G R A H V S A E A T L L A D D D P F A W G I R R Y -----	314	

SEQ ID NO: 7

Polypyrimidine rich region 	Splice leader acceptor sites Signal Peptide Polyadenylation site
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CCTTTTTCTTTTAAAAACAAAAAAATTCCGGGGGAATATGGAACAGGGTATAGGTAAAAGTGTCTGTCCCAAACAAAAAATTTTTT 90
M R K S V C P K Q K F F 12
TTTCCGCCTCCCATTTTTTTTGTGTGTTCCCTTGATCTCTCGAACAGGCAGGAAAGCTTCTGACCCAAATTTATAT 130
F S A F P F F F C V F P L I S R T G Q E K L L F D Q K Y 42
AAATTATTAAGGCAGAAAAGAAAAGAAAAAAATCAACGAGCAAACAGGAGAGAACACCAACAAAGGGAAATTATGCGATTT
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K I I K G E K K E K K N Q R A N R R E H Q Q K R E I M R F 72
AAGAAATCATTCACATGCACATGCACGGAAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTGCCACATCCAGGTTCGAAT 360
K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 102
ATGGCGGAGAAGAAAGCATACCTGCAGGAAACATGGATTTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT 430
M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F 132
GGAGCCTTTTATTGACCCTATTGAAGAAGGCCTGACTTGGGATGGTATTCATGGATCCGGTGGCTATTAAATATGTGTGGACAT 520
G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 162
HACTCAATTGCAGCGTTACGGCGCAGTTGAAACGGAATTGTGAGCGTGCCCGAAGGAAACAAATGTCCGGTGTCCGGACACA

N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T 510
CCTGCGGGTTGGTGCCGCGTACGGCACACCTCAGAGGGTTACTGAGAGGTGAGGTCAATGCACCTCATT 700
P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 222
TTGTATCAGCAGGATGTGGTGGTTGTGCCAAAGCCCATGGTGAAGTACGGGTATGGTGAATGGTACCCCTCATT

L Y Q Q D V V V V L P K P Y G E V R V D I A F G G N F F A I 252
GTTCCCGCGGAGCASTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTCCAGGAGGCAGGAGAACTCTCGGTACTGAACTCAAT 330
V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 232
CSCAGTGTGAAGGTTCAGCACCCCTCAGCTGCCCCCATTAACACTGTTGAGATATACGGTCCCGCAACGAACCCGGAGGA 970
R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312
AACTACAAAGGATGGTGATTTGGCAATCCGCAGGCGGATCGCCTCCAGTGGGACAGGGCACCCGCAAGATGGCAAACCTTT

Y X K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 1060
CCCAAGGGCAGCTCCGCATCGGAGAGACTTTGTGACCGAGCAACTCGGCTCACTTTCCAGGGCAGGGTACTTGGGGAGGGGGA

A S G Q L R I G E T F V Y E S I L G S L F Q G R V I G E E R 342
ATACCGGGGTGAAGGTGCGGTGACCAAGATGCCGAGGAAGGGATGCTCGTTCAACGGCAGGAAATTACTGGAAGGCTTTTTATCG

I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 402
GTTTCAACCCATCTGTTGACCAACGGATCCGTTAAAGAACCGATTCAATAAGGATAGTCTGGTAAGACAGAACTATT

G F N T M L F D P T D P F K N G F T I K Q * 423
GGGAACCGGTGCGAACAGGTGCTACGTGAACGGTATGAATCGTTTTTTTATTTTTTTATAGGTGCATT

ATTATTAAATTTTTTGGGTTCCACCGTACCGGTTGGAGCAGGGAAAGCATAGCGGCCGGACATTTTTGCTTTTAT

TTCATTTCATCTCCTACCCCCTGGTTCCACCGGGGGGTCTTGTGGTGGAGGTCTAAATCCGCACCTCG

AGGAATAACAATTTCAATTTCAATCTGGATCAAAAGGCAT 1600
1651

Obs : Underlined the sequenced peptides used to deduce degenerated primers for cloning

(d) Nucleotide sequence and peptide sequence TcPA45

SEQ ID NO. 8

M R K S V C P K Q K F F
 TTTTCCGCCCTCCCATT TTTTTGTGTGTTCCCTTGAATCTCTCGAACAGGGCAGGAAAAGCTTCTGTTGACCAAAATAAT
 F S A F P F F F C V F P L I S R T G Q E K L L F D Q K Y 160
 AAAATTATTAAGGGCGAGAAAAAGAAAAAGAAAAAATCAACGAGAACACGGAGAGAACACCAACAAAAAGGGAAATTATGCGATT
 K I I K G E K K K N Q R A N R R E H Q Q K R E I M R F 42
 AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCCACCGGATTGTGACGAGTGGTTGCCACACATTCCAGGTTCGAAT
 K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 270
 ATGGCGGAGAAGAAAGCATAACCTCGAGGAAAACATGGATTATTGAGCGTGGCATATGCTGGAACACACGTGGTCAATGATGATATGTT
 M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F 360
 GGAGCCTTTTATTGACCCATTGAAGAAGCGCTGACTTGGGCATGGTATTCAATGGATACCGGTGGCTATTAAATATGTTGACAT
 G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G K 132
 AACTCAATTGCGCGGTTACGGCGGCAAGTTGAAGACGGGAAATTGTGAGCGTGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA
 N S I A A V T A A V E T G I V S V P A K A T N V P V V L D T 520
 CCTGCGGGGTGGTGCACCGCACACCTCAGAGTGGTACTGAGAGTGAGGTGTCAATGCGACTTATTCATGTAACCCCTCAATT
 P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 162
 TTGTATCAGCAGGGATGGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCAATTGGAGGCAATTTCGCGATT
 L Y Q O D V V V V L P K P Y G E V R V D I A F G G N F F A I 610
 GTTCCCGGGAGCAGTGGGAAATTGATATCTCCGTCAAAACCTCTCCAGGCTGCAGGAGGAGACTTCTGCGTACTGAAATCAAT
 V P A E Q L G I D I S V Q N L M S R L Q E A G E L L R T E I N 192
 CGCAGTGTGAAGGTTCAAGCACCTCAGCTGCCCATATTAAACACTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 970
 R S V K V Q H P Q L P H I N T V D C V E I Y G P P T N P E A 312
 AACTACAAGAACGTTGTGATATTGGCAATGCCAGCCGGATCGCTCTCCATGTGGGACAGGCACCCAGGCCAACGATGGCAACACTTAT
 N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 1060
 GCCAAAGGCCAGCTTCGCATCGAGAGACTTTGTGTACCGAGAGCATACTCGGCTCACTCTCCAGGGCAGGGTACTTGGGGAGGAGGCA 342
 A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 1150
 ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTGTAAACGGCAGAAAATTACTGGAAAGGCTTTATCATT 372
 I P G V K V P V T K D A E E G M L V V T A E I T G K A F I M 1240
 GGTTCAACACCATGCTGTTGACCCAAACGGATCCGTTAAGAACGGATTCACTAAAGCAGTAGATCTGGTAGAGGCACAGGAAACTATT 402
 G F T T M L F D P T D P F K N G F T L K Q * 1330
 GGGGAACACGCTGCCAACAGGTGCTACGTGAAGGGTATTGAATGAAATGTTTTTTTATTTTATTTTATTTTATTTGATTAGTCATT 423
 ATTATTAATTTTTTTTGTGTTGGGTTCAACGGTACCGCTGGAGCAGGGAAAGCGATAGCGGGCCGACAAATTTTTGCTTTTAT 1420
 TTTCATTTTCACTTCCCTACCCAAACCCCTGGTCCACCGGTGCGGGGCTTGTGGCTGGAGGAGTCCTAAATCCCGCACCTCGG 1510
 AGGAATAACATATTTCATTTGAACTTCAGGCAACAGGTGCTACGTGAAGGGTATTGAATGAAATGTTTTTTTATTTTATTTTATTTGATTAGTCATT 1651

Polyadenylation site

Obs : Underlined the sequenced peptides used to deduce degenerated primers for cloning

(a) Nucleotide sequence and peptide sequence TcPA45

SEQ ID NO. 9

CGAACAGGGCAGGAAAGCTTCTGTTGACCAA AAATAT 270
 F S A F P F F F C V F P L I S R T G Q E K L L F D Q K Y 72
 AAAATTATAAGGGCGAGAAGAAAAGAAAAAAATCAACGAGCAGCAGGGAGAGAACACCAACAAAAAGGGAAATTATGCGATT 360
 K I I K G E K K E K K N Q R A N R R E H Q Q K R E I N R F 102
 AAGAAATCATTCACATGCATGCACATGCATACGGAAGGTGAGCAGCACGGATTGTGACGAGTGGTTGCCACACATTCCAGGGTCGAAT 430
 K K S F T C I D M H T E G E A A R I V T S G L P H I P G S N 132
 ATGGCGGAGAAGAACGACATCTGCAGGAAACATGGATTATTGAGGCAGTGGCATAATGCTGGAACACAGTGGTCATGATGATAFGTT 520
 M A E K K A Y L Q E N M D Y L R R G I M L E P R G H D D M F 162
 GGAGCCTTTTATTGACCCATTGAGAGAGCGCTGACTTGGGCATGGTATTCTGAGATAACGGTGGCTATTAAATAATGTTGGACAT 610
 G A F L F D P I E E G A D L G M V F M D T G G Y L N M C G H 192
 AACTCAATTGCAGCGGTTACGGCGCAGTTGAAACCGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCTGGACAC 700
 N S I A A V T A A V E T G I V S V P A K A T N V P V V L D - 222
 CCTCGGGGTTGGTGCACGGTACGGCACACCTCAGAGTGGTACTGAGAGTGGAGGTGTCAAATGCGAGTATTATCATTGACCGTACCTCATTT 730
 P A G L V R G T A H L Q S G T E S E V S N A S I I N V P S F 252
 TTGTATCAGCAGGATGTGGTGGTGTGCTGCAAGCCCTATGGTGAAGTACGGGTTGATATTGCAATTGGAGGCATTTTCGCCATT 330
 L Y Q O Q D V V V V L P K P Y G E V R V D I A F G G N F F A I 282
 GTTCCCGGGAGCAGTTGGAAATTGATATCTCCGTCACGGCTGCAGGAGGAGAACACTTCTGCGTACTGAAATCAATT 370
 V P A E Q L G I D I S V Q N L S R L Q E A G E L L R T E I N 312
 CGCAGTGTGAAGGTTCAGCACCCCTCAGCTGCCCATATTAAACTGTTGAGATAACGGTCCGGCAACGAAACCCGGAGGCA 1060
 R S V K V Q H P Q L P H I N T V D C V E Y I Y G P P T N P E A 342
 AACTACAAGAACGTTGTGATATTGCAATGCCAGGGCGATCGCTCTCCATGTGGACAGGCACCAGGCCAGATGGCAACACTTAT 1150
 N Y K N V V I F G N R Q A D R S P C G T G T S A K M A T L Y 372
 GCCAAAGGCCAGCTTCGCATCGAGAGACTTTGTGTACGAGAGCATACTCGGCTCACTCTCCAGGGCAGGGTACTTGGGACGGAGCGA 1240
 A K G Q L R I G E T F V Y E S I L G S L F Q G R V L G E E R 402
 ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG 1330
 I P G V K V P V T K D A E E G M L V T A E I T G K A F I M 423
 GGTTTCAACACCATCTGTTGACCCAACGGGATCCGTTAGAACCGGATTCACTTAAAGCAGTAGATCTGGTAGAGCAGAGAACCTATT 1420
 G F N T M L F D P T D P F K N G F T L K Q - 1510
 GGGGAACACGTCGAACAGGTGCTGCTACGTGAAGGGTATTGAAATGTTGGTTTTTTTATTTTTTATTTTTTATTTAGTGCATT 1600
 ATTATTAATTTTTTTTGTGTTGGGTTCAACGGTACCGCGTTGGGAGCAGGGAAAGCGATAACGGCCGGACARTTTTTGCTTTTAT 1650
 TTTCATTTTCACTTCCATACCCGACCCCCCTGGTCCACCGGTCGGGGGGTCTTGTGGAGGAGTCTAAATCCCGCACCTCGG
 AGGAATAAACATATTTCGATATTGCAACCTGGAACTCAACGGCAG

Polyadenylation site

Obs : Underlined the sequenced peptides used to deduce degenerated primers for cloning

(b) Nucleotide sequence and peptide sequence TcPA45

SEQUENCE ID NO:10

Signal peptide

M R K S V C P K Q K F F

Nucleotide sequence of signal sequence TcPA45

SEQUENCE ID NO:11

ATG CGA TTT <
K 2 9
360
333
430
222
320
162
610
292
703
222
750
222
660
312
312
1362
312
312
462
1312
432
1422
1512
1602
1622

Sequence ID NO:11

ATG CGA TTT <

K 2 9

360
333
430
222
320
162
610
292
703
222
750
222
660
312
312
1362
312
312
462
1312
432
1422
1512
1602
1622

SEQ ID NO : 12

5' TTICCRAADATIACIACGTT 3'

SEQ ID NO : 13

5' ATHGCITYGGIGGIAAYTTT 3'

SEQ ID NO : 14

5' TTICCRAADATIACIACGTT 3'

SEQ ID NO : 15

5' CTCTCCCATGGGGCAGGAAAAGCTTCTG 3'

SEQ ID NO : 16

5' CTGAGCTCGACCAGATCTATCTGC 3'

SEQ ID NO : 17

1 cctttttttt tttaaaaaca aaaaaaaattc cgggggggaat atggAACAGG GtataATGCGT
61 aaaagtgtct gtccccaaaca aaaaattttt tttcccgccc tcccatttttt tttttttttt
121 tgtgtgtttc ctttgatctc tcgaaacaggc caggaaaagc ttctgtttga ccaaaaatat
181 aaaattatta agggcgagaa aaaaagaaaaag aaaaaaaatc aacgagcaaa caggagagaa
241 caccAACACAA aaaggaaat tatgcgattt aagaatcat tcacatgcac cggacatgcac
301 acgaaaggcg aagcagcacg gattttgacg aatggtttgc cacacatttc aggtttcgaaat
361 atggcgaga agaaaagcata cctgcaggaa aacatggattt atttgaggcg tggcataatg
421 ctggAACCCAC gtggtcatga tgatztgtt ggagcctttt tatttgaccc tatttgaaagaa
481 ggcgttgact tgggcatttgtt attcatggat accgggtggct attttaaatac gttttggacat
541 aactcaatttgc cagcggttac ggcggcagt t gaaacgggaa ttgttgagcg t ggcggcgaag
601 gcaacaaatg ttcccggttgc cctggacaca cctgcgggggt tggtgccgcg tacggcacac
661 cttcagatgt gtactgagag tgagggttca aatgcgagta ttatcaatgt acccttcattt
721 ttgttatcgc aggatgttgtt ggttgttttgc ccaaaaggccc atgggtgaatg acgggttgtat
781 attgcatttg gaggcaattt tttccgcattt gttcccgccgg agcaatgttggg aatttgatatac
841 tccgttcaaa accttccag gctgcaggag gcaaggaaac ttctgtgtac taaaatcaat
901 cgcaatgtgtga aggttcagca ccctcagotg ccccatatttta acactgttggc ttgttgttgg
961 atatacggtc cgccaaacgaa cccggaggca aactacaaga acgttgttat attttggcaat
1021 cgccaggccgg atcgctctcc atgtgggaca ggcaccacgc ccaagatgc aacactttat
1081 gccaaaggcc agcttcgcac cggagagact tttgtgtacg agagcataact cggctcactic
1141 ttccaggccgaa gggtaacttgg ggaaggagcga ataccgggggg tggagggtggcc ggttgaccaaa
1201 gatggccgggg aagggtatgt cgttgtaaacg gcaagaaatttta ctggaaaggc ttttatcatg
1261 ggtttcaaca ccatgttgtt tgacccaaacg gatccgtttt aaaaacggatt cacattttaaag
1321 cagtagatct ggttagagcac agaaactttt gggaaacacgc tggcaacagg tggatgttacg
1381 tggagggtat tggatgtatc ttttttttt attttttttt tttttttttt ttagtgtatc
1441 attttttttt tttttttttt ttttgggggtt tcaacgggtac cgggtttggga gcaaggaaagc
1501 gatagcgccggcc ggacaattttt ttgtttttat tttcattttc atcttccttac ccaacccctt
1561 tggttccacc ggtcgccggcg gggtctttgtg ggtggaggag tccattttttcc cggccatctgg
1621 aggaataaaac atatttcaat ttcatatctt ggaatcaaaa ggcac

SEQ ID NO : 18

WIIK

SEQ ID NO : 19

IVTGSLPDISG

SEQ ID NO : 20

ATNVPVVLDTPAGLVR

SEQ ID NO : 21

VDIAFGGNF

SEQ ID NO : 22

NVVIFGNR

SEQ ID NO : 23

MATLYAK

SEQ ID NO : 24

5' TCCGTATCCATGTCGATGC 3'

SEQ ID NO : 25

5' TATTATTGATAACAGTTCTG 3'

SEQ ID NO : 26

5' CTCTCCCATGGGCAGGAAAAGCTTCTG 3'